

PCT09

RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/701,080A

TIME: 13:05:35

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\12212001\I701080A.raw

P.5

3 <110> APPLICANT: O'CONNOR, MARK J.
 4 ZIMMERMAN, HOLGER
 6 <120> TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN
 P300 FOR USE IN
 7 TRANSCRIPTIONAL REGULATION
 9 <130> FILE REFERENCE: 117-328
 11 <140> CURRENT APPLICATION NUMBER: US 09/701,080A
 12 <141> CURRENT FILING DATE: 2001-02-27
 14 <150> PRIOR APPLICATION NUMBER: GB 9811303.8
 15 <151> PRIOR FILING DATE: 1998-05-26
 17 <150> PRIOR APPLICATION NUMBER: GB 9900157.0
 18 <151> PRIOR FILING DATE: 1999-01-05
 20 <160> NUMBER OF SEQ ID NOS: 36
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 13
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from E1A
 33 <400> SEQUENCE: 1
 34 Val Asn Glu Phe Phe Pro Glu Ser Leu Ile Leu Ala Ala
 35 1 5 10
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 11
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from E1A
 45 <400> SEQUENCE: 2
 46 Val Asn Glu Phe Phe Pro Ala Ser Ala Ile Leu
 47 1 5 10
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 11
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Artificial Sequence
 54 <220> FEATURE:
 55 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from E1A
 58 <400> SEQUENCE: 3
 59 Val Asn Glu Phe Ala Pro Ala Ser Ala Ile Ala
 60 1 5 10
 62 <210> SEQ ID NO: 4
 63 <211> LENGTH: 13
 64 <212> TYPE: PRT
 65 <213> ORGANISM: Artificial Sequence
 67 <220> FEATURE:
 68 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from p53
 70 <400> SEQUENCE: 4

ENTERED

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71 Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro
72   1               5               10
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 13
76 <212> TYPE: PRT
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from E2F
82 <400> SEQUENCE: 5
83 Phe Asp Cys Asp Phe Gly Asp Leu Thr Pro Leu Asp Phe
84   1               5               10
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 19
89 <212> TYPE: PRT
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from Mdm-2
95 <400> SEQUENCE: 6
96 Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln Pro
97   1               5               10               15
99 Ile Gln Met
101 <210> SEQ ID NO: 7
102 <211> LENGTH: 19
103 <212> TYPE: PRT
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from CBP
109 <400> SEQUENCE: 7
110 Gly Cys Lys Arg Lys Thr Asn Gly Gly Cys Pro Val Cys Lys Gln Leu
111   1               5               10               15
113 Ile Ala Leu
115 <210> SEQ ID NO: 8
116 <211> LENGTH: 13
117 <212> TYPE: PRT
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from E1A
123 <400> SEQUENCE: 8
124 Val Asn Glu Phe Phe Pro Glu Ser Leu Ile Leu Ala Ala
125   1               5               10
127 <210> SEQ ID NO: 9
128 <211> LENGTH: 13
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from p53
135 <400> SEQUENCE: 9
136 Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro
137   1               5               10

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139 <210> SEQ ID NO: 10
140 <211> LENGTH: 13
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from E2F
147 <400> SEQUENCE: 10
148 Phe Asp Cys Asp Phe Gly Asp Leu Thr Pro Leu Asp Phe
149   1           5           10
151 <210> SEQ ID NO: 11
152 <211> LENGTH: 13
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from TFIIB
159 <400> SEQUENCE: 11
160 Met Met Asn Ala Phe Lys Glu Ile Thr Thr Met Ala Asp
161   1           5           10
163 <210> SEQ ID NO: 12
164 <211> LENGTH: 13
165 <212> TYPE: PRT
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from YY1
171 <400> SEQUENCE: 12
172 Ala Glu Asp Gly Phe Glu Asp Gln Ile Leu Ile Pro Val
173   1           5           10
175 <210> SEQ ID NO: 13
176 <211> LENGTH: 13
177 <212> TYPE: PRT
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from YY1
183 <400> SEQUENCE: 13
184 Cys Thr Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys
185   1           5           10
187 <210> SEQ ID NO: 14
188 <211> LENGTH: 13
189 <212> TYPE: PRT
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from YY1
195 <400> SEQUENCE: 14
196 Cys Gly Lys Ala Phe Val Glu Ser Ser Lys Leu Lys Arg
197   1           5           10
199 <210> SEQ ID NO: 15
200 <211> LENGTH: 13
201 <212> TYPE: PRT
202 <213> ORGANISM: Artificial Sequence

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204 <220> FEATURE:
205 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from MyoD
207 <400> SEQUENCE: 15
208 Thr Thr Asp Asp Phe Tyr Asp Asp Pro Cys Phe Asp Ser
209   1               5               10
211 <210> SEQ ID NO: 16
212 <211> LENGTH: 19
213 <212> TYPE: PRT
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from CBP
219 <400> SEQUENCE: 16
220 Gly Cys Lys Arg Lys Thr Asn Gly Gly Cys Pro Val Cys Lys Gln Leu
221   1               5               10               15
223 Ile Ala Leu
225 <210> SEQ ID NO: 17
226 <211> LENGTH: 19
227 <212> TYPE: PRT
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Description of Artificial Sequence:derived from p300
233 <400> SEQUENCE: 17
234 Gly Cys Lys Arg Lys Thr Asn Gly Gly Cys Pro Ile Cys Lys Gln Leu
235   1               5               10               15
237 Ile Ala Leu
239 <210> SEQ ID NO: 18
240 <211> LENGTH: 151
241 <212> TYPE: PRT
242 <213> ORGANISM: Human papillomavirus
244 <400> SEQUENCE: 18
245 Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu Pro Gln Leu Cys
246   1               5               10               15
248 Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val Tyr
249   20               25               30
251 Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe Arg
252   35               40               45
254 Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys Asp
255   50               55               60
257 Lys Cys Leu Lys Phe Tyr Ser Lys Tyr Ser Glu Tyr Arg His Tyr Cys
258   65               70               75               80
260 Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro Leu
261   85               90               95
263 Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys Pro
264   100              105              110
266 Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn Ile
267   115              120              125
269 Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg
270   130              135              140
272 Thr Arg Arg Glu Thr Gln Leu

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273 145 150

275 <210> SEQ ID NO: 19

276 <211> LENGTH: 49

277 <212> TYPE: DNA

278 <213> ORGANISM: Artificial Sequence

280 <220> FEATURE:

281 <223> OTHER INFORMATION: Description of Artificial Sequence: polylinker of plasmid

pMALP

283 <400> SEQUENCE: 19

284 ggatccgctg acctcgagcc cgggctgcag aagcttgatt gattagctt 49

286 <210> SEQ ID NO: 20

287 <211> LENGTH: 12

288 <212> TYPE: PRT

289 <213> ORGANISM: Artificial Sequence

291 <220> FEATURE:

292 <221> NAME/KEY: VARIANT

293 <222> LOCATION: (1)

294 <223> OTHER INFORMATION: Xaa represents Lys or Arg

296 <220> FEATURE:

297 <221> NAME/KEY: VARIANT

298 <222> LOCATION: (2)

299 <223> OTHER INFORMATION: Xaa represents Lys or Arg

301 <220> FEATURE:

302 <221> NAME/KEY: VARIANT

303 <222> LOCATION: (3)

304 <223> OTHER INFORMATION: Xaa represents any amino acid

306 <220> FEATURE:

307 <221> NAME/KEY: VARIANT

308 <222> LOCATION: (5)

309 <223> OTHER INFORMATION: Xaa represents any amino acid

311 <220> FEATURE:

312 <221> NAME/KEY: VARIANT

313 <222> LOCATION: (6)

314 <223> OTHER INFORMATION: Xaa represents any amino acid

316 <220> FEATURE:

317 <221> NAME/KEY: VARIANT

318 <222> LOCATION: (9)

319 <223> OTHER INFORMATION: Xaa is Val or Ile

321 <220> FEATURE:

322 <221> NAME/KEY: VARIANT

323 <222> LOCATION: (11)

324 <223> OTHER INFORMATION: Xaa represents Lys or Arg

326 <220> FEATURE:

327 <221> NAME/KEY: VARIANT

328 <222> LOCATION: (12)

329 <223> OTHER INFORMATION: Xaa represents any amino acid

331 <220> FEATURE:

332 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus sequence of transcriptional adaptor

333 motif (TRAM)

335 <400> SEQUENCE: 20

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21

L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22

12/21/01 13:05:36